Raymond C Stevens

List of Publications by Year
in descending order

414 papers	55,422 citations	950 115 h-index	1385 222 g-index
430 all docs	430 docs citations	430 times ranked	35912 citing authors

#	Article	IF	Citations
1	High-Resolution Crystal Structure of an Engineered Human Î² ₂ -Adrenergic G Proteinâ€“Coupled Receptor. Science, 2007, 318, 1258-1265.	6.0	3,112
2	The 2.6 Angstrom Crystal Structure of a Human A _{2A} Adenosine Receptor Bound to an Antagonist. Science, 2008, 322, 1211-1217.	6.0	1,688
3	Structures of the CXCR4 Chemokine GPCR with Small-Molecule and Cyclic Peptide Antagonists. Science, 2010, 330, 1066-1071.	6.0	1,610
4	GPCR Engineering Yields High-Resolution Structural Insights into Î² ₂ -Adrenergic Receptor Function. Science, 2007, 318, 1266-1273.	6.0	1,324
5	Influenza Neuraminidase Inhibitors Possessing a Novel Hydrophobic Interaction in the Enzyme Active Site:Â Design, Synthesis, and Structural Analysis of Carbocyclic Sialic Acid Analogues with Potent Anti-Influenza Activity. Journal of the American Chemical Society, 1997, 119, 681-690.	6.6	1,061
6	Structure of the Human Dopamine D3 Receptor in Complex with a D2/D3 Selective Antagonist. Science, 2010, 330, 1091-1095.	6.0	1,034
7	Structure-Function of the G Proteinâ€“Coupled Receptor Superfamily. Annual Review of Pharmacology and Toxicology, 2013, 53, 531-556.	4.2	907
8	A Specific Cholesterol Binding Site Is Established by the 2.8 Ã... Structure of the Human Î²2-Adrenergic Receptor. Structure, 2008, 16, 897-905.	1.6	892
9	Structural Basis for Allosteric Regulation of GPCRs by Sodium Ions. Science, 2012, 337, 232-236.	6.0	860
10	Structure of the human Î¼-opioid receptor in complex with JDTic. Nature, 2012, 485, 327-332.	13.7	797
11	Structure of an Agonist-Bound Human A _{2A} Adenosine Receptor. Science, 2011, 332, 322-327.	6.0	783
12	Protein production and purification. Nature Methods, 2008, 5, 135-146.	9.0	763
13	Structure of the human histamine H1 receptor complex with doxepin. Nature, 2011, 475, 65-70.	13.7	727
14	Crystal structure of botulinum neurotoxin type A and implications for toxicity. Nature Structural Biology, 1998, 5, 898-902.	9.7	687
15	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. Nature, 2015, 523, 561-567.	13.7	683
16	Biased Signaling Pathways in Î² ₂ -Adrenergic Receptor Characterized by ¹⁹ F-NMR. Science, 2012, 335, 1106-1110.	6.0	618
17	Structure of the CCR5 Chemokine Receptorâ€“HIV Entry Inhibitor Maraviroc Complex. Science, 2013, 341, 1387-1390.	6.0	606
18	Crystal Structure of a Lipid G Proteinâ€“Coupled Receptor. Science, 2012, 335, 851-855.	6.0	600

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19	Structural Features for Functional Selectivity at Serotonin Receptors. Science, 2013, 340, 615-619.	6.0	600
20	Structural Insights into the Evolution of an Antibody Combining Site. Science, 1997, 276, 1665-1669.	6.0	572
21	Lipidic cubic phase injector facilitates membrane protein serial femtosecond crystallography. Nature Communications, 2014, 5, 3309.	5.8	505
22	Structure of a Class C GPCR Metabotropic Glutamate Receptor 1 Bound to an Allosteric Modulator. Science, 2014, 344, 58-64.	6.0	476
23	Structural Adaptations in a Membrane Enzyme That Terminates Endocannabinoid Signaling. Science, 2002, 298, 1793-1796.	6.0	473
24	Crystal Structure of the Human Cannabinoid Receptor CB1. Cell, 2016, 167, 750-762.e14.	13.5	468
25	Structural Basis for Molecular Recognition at Serotonin Receptors. Science, 2013, 340, 610-614.	6.0	454
26	Molecular control of Î´-opioid receptor signalling. Nature, 2014, 506, 191-196.	13.7	432
27	Structure of the nociceptin/orphanin FQ receptor in complex with a peptide mimetic. Nature, 2012, 485, 395-399.	13.7	430
28	Serial Femtosecond Crystallography of G Proteinâ€“Coupled Receptors. Science, 2013, 342, 1521-1524.	6.0	424
29	How Ligands Illuminate GPCR Molecular Pharmacology. Cell, 2017, 170, 414-427.	13.5	419
30	Allosteric sodium in class A GPCR signaling. Trends in Biochemical Sciences, 2014, 39, 233-244.	3.7	417
31	Structure of the human smoothened receptor bound to an antitumour agent. Nature, 2013, 497, 338-343.	13.7	415
32	Diversity and modularity of G protein-coupled receptor structures. Trends in Pharmacological Sciences, 2012, 33, 17-27.	4.0	403
33	Microscale Fluorescent Thermal Stability Assay for Membrane Proteins. Structure, 2008, 16, 351-359.	1.6	402
34	Discovery and Characterization of a Highly Selective FAAH Inhibitor that Reduces Inflammatory Pain. Chemistry and Biology, 2009, 16, 411-420.	6.2	401
35	Structural genomics of the Thermotoga maritima proteome implemented in a high-throughput structure determination pipeline. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11664-11669.	3.3	397
36	Ultrasensitive magnetic biosensor for homogeneous immunoassay. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 14268-14272.	3.3	387

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37	Generic GPCR residue numbers â€“ aligning topology maps while minding the gaps. Trends in Pharmacological Sciences, 2015, 36, 22-31.	4.0	387
38	Crystal structures of agonist-bound human cannabinoid receptor CB1. Nature, 2017, 547, 468-471.	13.7	379
39	Fusion Partner Toolchest for the Stabilization and Crystallization of G Protein-Coupled Receptors. Structure, 2012, 20, 967-976.	1.6	367
40	Severe acute respiratory syndrome coronavirus papain-like protease: Structure of a viral deubiquitinating enzyme. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5717-5722.	3.3	356
41	Structure of the human glucagon class B G-protein-coupled receptor. Nature, 2013, 499, 444-449.	13.7	352
42	Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. Cell, 2017, 170, 457-469.e13.	13.5	344
43	Conserved Binding Mode of Human Î²₂ Adrenergic Receptor Inverse Agonists and Antagonist Revealed by X-ray Crystallography. Journal of the American Chemical Society, 2010, 132, 11443-11445.	6.6	342
44	Common activation mechanism of class A GPCRs. ELife, 2019, 8, .	2.8	339
45	Structure of the human P2Y12 receptor in complex with an antithrombotic drug. Nature, 2014, 509, 115-118.	13.7	330
46	Crystal structure of the chemokine receptor CXCR4 in complex with a viral chemokine. Science, 2015, 347, 1117-1122.	6.0	325
47	Cholera Toxin Binding Affinity and Specificity for Gangliosides Determined by Surface Plasmon Resonanceâ€. Biochemistry, 1996, 35, 6375-6384.	1.2	321
48	Structure of the Angiotensin Receptor Revealed by Serial Femtosecond Crystallography. Cell, 2015, 161, 833-844.	13.5	315
49	Two disparate ligand-binding sites in the human P2Y1 receptor. Nature, 2015, 520, 317-321.	13.7	305
50	Sequence homology and structural analysis of the clostridial neurotoxins. Journal of Molecular Biology, 1999, 291, 1091-1104.	2.0	303
51	Structureâ^'Activity Relationship Studies of Novel Carbocyclic Influenza Neuraminidase Inhibitors. Journal of Medicinal Chemistry, 1998, 41, 2451-2460.	2.9	301
52	Structure of the Nanobody-Stabilized Active State of the Kappa Opioid Receptor. Cell, 2018, 172, 55-67.e15.	13.5	299
53	Agonist-bound structure of the human P2Y12 receptor. Nature, 2014, 509, 119-122.	13.7	279
54	Status of GPCR Modeling and Docking as Reflected by Community-wide GPCR Dock 2010 Assessment. Structure, 2011, 19, 1108-1126.	1.6	269

#	Article	IF	Citations
55	Crystal Structure of the Human Cannabinoid Receptor CB2. Cell, 2019, 176, 459-467.e13.	13.5	268
56	Community-wide assessment of GPCR structure modelling and ligand docking: GPCR Dock 2008. Nature Reviews Drug Discovery, 2009, 8, 455-463.	21.5	260
57	The GPCR Network: a large-scale collaboration to determine human GPCR structure and function. Nature Reviews Drug Discovery, 2013, 12, 25-34.	21.5	252
58	Crystal structure of tyrosine hydroxylase at 2.3 Ã... and its implications for inherited neurodegenerative diseases. Nature Structural Biology, 1997, 4, 578-585.	9.7	244
59	A â€˜litmus testâ€™ for molecular recognition using artificial membranes. Chemistry and Biology, 1996, 3, 113-120.	6.2	236
60	Structure-Based Discovery of Novel Chemotypes for Adenosine A_{2A} Receptor Antagonists. Journal of Medicinal Chemistry, 2010, 53, 1799-1809.	2.9	231
61	An approach to rapid protein crystallization using nanodroplets. Journal of Applied Crystallography, 2002, 35, 278-281.	1.9	227
62	Predicting the emergence of antibiotic resistance by directed evolution and structural analysis. Nature Structural Biology, 2001, 8, 238-242.	9.7	223
63	High-throughput protein crystallization. Current Opinion in Structural Biology, 2000, 10, 558-563.	2.6	221
64	Structure of CC chemokine receptor 2 with orthosteric and allosteric antagonists. Nature, 2016, 540, 458-461.	13.7	220
65	Insights into the structure of class B GPCRs. Trends in Pharmacological Sciences, 2014, 35, 12-22.	4.0	218
66	Crystal structure of the anti-viral APOBEC3G catalytic domain and functional implications. Nature, 2008, 456, 121-124.	13.7	213
67	Design of high-throughput methods of protein production for structural biology. Structure, 2000, 8, R177-R185.	1.6	208
68	Structural basis for Smoothened receptor modulation and chemoresistance to anticancer drugs. Nature Communications, 2014, 5, 4355.	5.8	208
69	Structural basis of autoregulation of phenylalanine hydroxylase. Nature Structural Biology, 1999, 6, 442-448.	9.7	199
70	Global Efforts in Structural Genomics. Science, 2001, 294, 89-92.	6.0	195
71	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. Nature, 2017, 546, 312-315.	13.7	192
72	Structural basis of cell surface receptor recognition by botulinum neurotoxin B. Nature, 2006, 444, 1096-1100.	13.7	190

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73	Crystal Structure-Based Virtual Screening for Fragment-like Ligands of the Human Histamine H₁ Receptor. Journal of Medicinal Chemistry, 2011, 54, 8195-8206.	2.9	189
74	5-HT2C Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. Cell, 2018, 172, 719-730.e14.	13.5	185
75	Sphingosine-1-Phosphate and Its Receptors: Structure, Signaling, and Influence. Annual Review of Biochemistry, 2013, 82, 637-662.	5.0	184
76	Discovery of New GPCR Biology: One Receptor Structure at a Time. Structure, 2009, 17, 8-14.	1.6	180
77	Structure of the full-length glucagon class B G-protein-coupled receptor. Nature, 2017, 546, 259-264.	13.7	179
78	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic Î² Cell. Cell, 2018, 173, 11-19.	13.5	179
79	Charge-Induced Chromatic Transition of Amino Acid-Derivatized Polydiacetylene Liposomes. Langmuir, 1998, 14, 1974-1976.	1.6	177
80	Structural Basis of Severe Acute Respiratory Syndrome Coronavirus ADP-Ribose-1â€³-Phosphate Dephosphorylation by a Conserved Domain of nsP3. Structure, 2005, 13, 1665-1675.	1.6	175
81	Structural basis for selectivity and diversity in angiotensin II receptors. Nature, 2017, 544, 327-332.	13.7	174
82	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A2A Adenosine Receptor. Cell, 2018, 172, 68-80.e12.	13.5	173
83	Immunological Origins of Binding and Catalysis in a Diels-Alderase Antibody. Science, 1998, 279, 1929-1933.	6.0	172
84	Crystal Structure of Antagonist Bound Human Lysophosphatidic Acid Receptor 1. Cell, 2015, 161, 1633-1643.	13.5	169
85	Structural Insight into the Aromatic Amino Acid Hydroxylases and Their Disease-Related Mutant Forms. Chemical Reviews, 1999, 99, 2137-2160.	23.0	167
86	Proteomics Analysis Unravels the Functional Repertoire of Coronavirus Nonstructural Protein 3. Journal of Virology, 2008, 82, 5279-5294.	1.5	167
87	Molecular evolution of antibody cross-reactivity for two subtypes of type A botulinum neurotoxin. Nature Biotechnology, 2007, 25, 107-116.	9.4	165
88	Modulating Artificial Membrane Morphology:Â pH-Induced Chromatic Transition and Nanostructural Transformation of a Bolaamphiphilic Conjugated Polymer from Blue Helical Ribbons to Red Nanofibers. Journal of the American Chemical Society, 2001, 123, 3205-3213.	6.6	164
89	Three-Dimensional Structure of Human Tryptophan Hydroxylase and Its Implications for the Biosynthesis of the Neurotransmitters Serotonin and Melatoninâ€,â€¡. Biochemistry, 2002, 41, 12569-12574.	1.2	164
90	Crystal structure of the catalytic domain of human phenylalanine hydroxylase reveals the structural basis for phenylketonuria. Nature Structural Biology, 1997, 4, 995-1000.	9.7	162

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91	Genetically Encoded Chemical Probes in Cells Reveal the Binding Path of Urocortin-I to CRF Class B GPCR. Cell, 2013, 155, 1258-1269.	13.5	159
92	Automation of X-ray crystallography. Nature Structural Biology, 2000, 7, 973-977.	9.7	158
93	Molecular genetics of tetrahydrobiopterin-responsive phenylalanine hydroxylase deficiency. Human Mutation, 2008, 29, 167-175.	1.1	158
94	From The Cover: Correction of kinetic and stability defects by tetrahydrobiopterin in phenylketonuria patients with certain phenylalanine hydroxylase mutations. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16903-16908.	3.3	156
95	Structural basis for bifunctional peptide recognition at human Î´-opioid receptor. Nature Structural and Molecular Biology, 2015, 22, 265-268.	3.6	151
96	Crystal Structure of Botulinum Neurotoxin Type A in Complex with the Cell Surface Co-Receptor GT1bâ€"Insight into the Toxinâ€"Neuron Interaction. PLoS Pathogens, 2008, 4, e1000129.	2.1	150
97	Advances in GPCR Modeling Evaluated by the GPCR Dock 2013 Assessment: Meeting New Challenges. Structure, 2014, 22, 1120-1139.	1.6	149
98	Structure of CC Chemokine Receptor 5 with a Potent Chemokine Antagonist Reveals Mechanisms of Chemokine Recognition and Molecular Mimicry by HIV. Immunity, 2017, 46, 1005-1017.e5.	6.6	148
99	Structural Basis for Ligand Recognition and Functional Selectivity at Angiotensin Receptor. Journal of Biological Chemistry, 2015, 290, 29127-29139.	1.6	145
100	Rastering strategy for screening and centring of microcrystal samples of human membrane proteins with a sub-10 Âµm size X-ray synchrotron beam. Journal of the Royal Society Interface, 2009, 6, S587-97.	1.5	144
101	Rapid refinement of crystallographic protein construct definition employing enhanced hydrogen/deuterium exchange MS. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 751-756.	3.3	141
102	Structural consequences of effector binding to the T state of aspartate carbamoyltransferase: crystal structures of the unligated and ATP- and CTP-complexed enzymes at 2.6-.ANG. resolution. Biochemistry, 1990, 29, 7691-7701.	1.2	140
103	Crystal Structure of Tyrosine Hydroxylase with Bound Cofactor Analogue and Iron at 2.3 Ã… Resolution:â€‰ Self-Hydroxylation of Phe300 and the Pterin-Binding Site,. Biochemistry, 1998, 37, 13437-13445.	1.2	140
104	Structural basis of ligand recognition at the human MT1 melatonin receptor. Nature, 2019, 569, 284-288.	13.7	140
105	Structure of Tetrameric Human Phenylalanine Hydroxylase and Its Implications for Phenylketonuria. Journal of Biological Chemistry, 1998, 273, 16962-16967.	1.6	137
106	Structural Connection between Activation Microswitch and Allosteric Sodium Site in GPCR Signaling. Structure, 2018, 26, 259-269.e5.	1.6	134
107	The Structural Basis of Phenylketonuria. Molecular Genetics and Metabolism, 1999, 68, 103-125.	0.5	132
108	Structure-guided inhibitor design for human FAAH by interspecies active site conversion. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12820-12824.	3.3	132

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109	Ligand-Dependent Perturbation of the Conformational Ensemble for the GPCR Î²2 Adrenergic Receptor Revealed by HDX. Structure, 2011, 19, 1424-1432.	1.6	129
110	Coupling of an induced fit enzyme to polydiacetylene thin films: Colorimetric detection of glucose. Advanced Materials, 1997, 9, 481-483.	11.1	128
111	Steroid-based facial amphiphiles for stabilization and crystallization of membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1203-11.	3.3	127
112	Ribonucleocapsid Formation of Severe Acute Respiratory Syndrome Coronavirus through Molecular Action of the N-Terminal Domain of N Protein. Journal of Virology, 2007, 81, 3913-3921.	1.5	125
113	Stabilization of the Human Î²2-Adrenergic Receptor TM4â€“TM3â€“TM5 Helix Interface by Mutagenesis of Glu1223.41, A Critical Residue in GPCR Structure. Journal of Molecular Biology, 2008, 376, 1305-1319.	2.0	125
114	PAHdb 2003: What a locus-specific knowledgebase can do. Human Mutation, 2003, 21, 333-344.	1.1	124
115	A Structural Perspective of the Sequence Variability Within Botulinum Neurotoxin Subtypes A1-A4. Journal of Molecular Biology, 2006, 362, 733-742.	2.0	122
116	Biophysical Characterization of the Stability of the 150-Kilodalton Botulinum Toxin, the Nontoxic Component, and the 900-Kilodalton Botulinum Toxin Complex Species. Infection and Immunity, 1998, 66, 2420-2425.	1.0	121
117	Cocrystal structure of synaptobrevin-II bound to botulinum neurotoxin type B at 2.0 A resolution. , 2000, 7, 687-692.		119
118	An electrostatic mechanism for Ca2+-mediated regulation of gap junction channels. Nature Communications, 2016, 7, 8770.	5.8	119
119	The genesis of high-throughput structure-based drug discovery using protein crystallography. Current Opinion in Chemical Biology, 2002, 6, 704-710.	2.8	118
120	The Role of a Sodium Ion Binding Site in the Allosteric Modulation of the A2A Adenosine G Protein-Coupled Receptor. Structure, 2013, 21, 2175-2185.	1.6	118
121	Concept of the H(Î´+)â‹¯ H(Î´â€“) interaction. A low-temperature neutron diffraction study of cis-[IrH(OH)(PMe3)4]PF6. Journal of the Chemical Society Dalton Transactions, 1990, , 1429-1432.	1.1	117
122	Structural Plasticity and the Evolution of Antibody Affinity and Specificity. Journal of Molecular Biology, 2003, 330, 651-656.	2.0	116
123	Dynamics of the Î²₂-Adrenergic G-Protein Coupled Receptor Revealed by Hydrogenâ^'Deuterium Exchange. Analytical Chemistry, 2010, 82, 1100-1108.	3.2	115
124	Time-Controlled Microfluidic Seeding in nL-Volume Droplets To Separate Nucleation and Growth Stages of Protein Crystallization. Angewandte Chemie - International Edition, 2006, 45, 8156-8160.	7.2	113
125	Constitutive phospholipid scramblase activity of a G protein-coupled receptor. Nature Communications, 2014, 5, 5115.	5.8	112
126	Blue-Fluorescent Antibodies. Science, 2000, 290, 307-313.	6.0	110

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127	Crystal Structure of Nonstructural Protein 10 from the Severe Acute Respiratory Syndrome Coronavirus Reveals a Novel Fold with Two Zinc-Binding Motifs. Journal of Virology, 2006, 80, 7894-7901.	1.5	110
128	Engineered nanostructured Î²-sheet peptides protect membrane proteins. Nature Methods, 2013, 10, 759-761.	9.0	110
129	Conformational states of the full-length glucagon receptor. Nature Communications, 2015, 6, 7859.	5.8	110
130	Mechanisms underlying responsiveness to tetrahydrobiopterin in mild phenylketonuria mutations. Human Mutation, 2004, 24, 388-399.	1.1	109
131	Extending the Structural View of Class B GPCRs. Trends in Biochemical Sciences, 2017, 42, 946-960.	3.7	109
132	Structure of the glucagon receptor in complex with a glucagon analogue. Nature, 2018, 553, 106-110.	13.7	109
133	An online resource for GPCR structure determination and analysis. Nature Methods, 2019, 16, 151-162.	9.0	108
134	Crystal Structure and Site-Specific Mutagenesis of Pterin-Bound Human Phenylalanine Hydroxylaseâ€,â€¡. Biochemistry, 2000, 39, 2208-2217.	1.2	106
135	XFEL structures of the human MT2 melatonin receptor reveal the basis of subtype selectivity. Nature, 2019, 569, 289-292.	13.7	106
136	Preclinical evaluation of multiple species of PEGylated recombinant phenylalanine ammonia lyase for the treatment of phenylketonuria. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20894-20899.	3.3	105
137	Crystal structures of aspartate carbamoyltransferase ligated with phosphonoacetamide, malonate, and CTP or ATP at 2.8-.ANG. resolution and neutral pH. Biochemistry, 1990, 29, 7702-7715.	1.2	104
138	Automated Sample Mounting and Alignment System for Biological Crystallography at a Synchrotron Source. Structure, 2004, 12, 537-545.	1.6	104
139	Protein Biophysical Properties that Correlate with Crystallization Success in Thermotoga maritima: Maximum Clustering Strategy for Structural Genomics. Journal of Molecular Biology, 2004, 344, 977-991.	2.0	102
140	The interplay between binding energy and catalysis in the evolution of a catalytic antibody. Nature, 1997, 389, 271-275.	13.7	101
141	Structural basis of ligand binding modes at the neuropeptide Y Y1 receptor. Nature, 2018, 556, 520-524.	13.7	100
142	Designing Facial Amphiphiles for the Stabilization of Integral Membrane Proteins. Angewandte Chemie - International Edition, 2007, 46, 7023-7025.	7.2	99
143	Native phasing of x-ray free-electron laser data for a G proteinâ€“coupled receptor. Science Advances, 2016, 2, e1600292.	4.7	97
144	Structural Basis for Apelin Control of the Human Apelin Receptor. Structure, 2017, 25, 858-866.e4.	1.6	96

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145	A _{2A} adenosine receptor functional states characterized by ¹⁹ F-NMR. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12733-12738.	3.3	96
146	Crystal Structure of Fatty Acid Amide Hydrolase Bound to the Carbamate Inhibitor URB597: Discovery of a Deacylating Water Molecule and Insight into Enzyme Inactivation. Journal of Molecular Biology, 2010, 400, 743-754.	2.0	92
147	Determination of the melanocortin-4 receptor structure identifies Ca ²⁺ as a cofactor for ligand binding. Science, 2020, 368, 428-433.	6.0	89
148	Amino Acid Terminated Polydiacetylene Lipid Microstructures:Â Morphology and Chromatic Transition. Langmuir, 2000, 16, 5333-5342.	1.6	88
149	Single-molecule view of basal activity and activation mechanisms of the G protein-coupled receptor Î² ₂ AR. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14254-14259.	3.3	87
150	Nucleotides Acting at P2Y Receptors: Connecting Structure and Function. Molecular Pharmacology, 2015, 88, 220-230.	1.0	86
151	Shotgun crystallization strategy for structural genomics: an optimized two-tiered crystallization screen against theThermotoga maritimaproteome. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1028-1037.	2.5	85
152	A fully integrated protein crystallization platform for small-molecule drug discovery. Journal of Structural Biology, 2003, 142, 207-217.	1.3	84
153	Binding and Inactivation Mechanism of a Humanized Fatty Acid Amide Hydrolase by Î±-Ketoheterocycle Inhibitors Revealed from Cocrystal Structures. Journal of the American Chemical Society, 2009, 131, 10497-10506.	6.6	83
154	Ligand Binding and Subtype Selectivity of the Human A2A Adenosine Receptor. Journal of Biological Chemistry, 2010, 285, 13032-13044.	1.6	83
155	Full-length human GLP-1 receptor structure without orthosteric ligands. Nature Communications, 2020, 11, 1272.	5.8	83
156	Expression and Purification of the Saccharomyces cerevisiae Î±-Factor Receptor (Ste2p), a 7-Transmembrane-segment G Protein-coupled Receptor. Journal of Biological Chemistry, 1997, 272, 15553-15561.	1.6	81
157	In situdata collection and structure refinement from microcapillary protein crystallization. Journal of Applied Crystallography, 2005, 38, 900-905.	1.9	81
158	NMR screening and crystal quality of bacterially expressed prokaryotic and eukaryotic proteins in a structural genomics pipeline. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1901-1905.	3.3	81
159	Fluorine-19 NMR of integral membrane proteins illustrated with studies of GPCRs. Current Opinion in Structural Biology, 2013, 23, 740-747.	2.6	81
160	Crystal structure of a multi-domain human smoothened receptor in complex with a super stabilizing ligand. Nature Communications, 2017, 8, 15383.	5.8	81
161	Elucidating the active Î´-opioid receptor crystal structure with peptide and small-molecule agonists. Science Advances, 2019, 5, eaax9115.	4.7	81
162	Organometallic chemistry. 22. Triphenylsilyl perchlorate revisited: silicon-29 and chlorine-35 NMR spectroscopy and x-ray crystallography showing covalent nature in both solution and the solid state. Difficulties in observing long-lived silyl cations in the condensed state. Journal of the American Chemical Society, 1987, 109, 5123-5126.	6.6	80

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163	Crystal Structure of a Monomeric Form of Severe Acute Respiratory Syndrome Coronavirus Endonuclease nsp15 Suggests a Role for Hexamerization as an Allosteric Switch. Journal of Virology, 2007, 81, 6700-6708.	1.5	80
164	GPCR stabilization using the bicelle-like architecture of mixed sterol-detergent micelles. Methods, 2011, 55, 310-317.	1.9	80
165	NMR structure and dynamics of the agonist dynorphin peptide bound to the human kappa opioid receptor. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11852-11857.	3.3	80
166	Agonists for 13 Trace Amine-Associated Receptors Provide Insight into the Molecular Basis of Odor Selectivity. ACS Chemical Biology, 2012, 7, 1184-1189.	1.6	79
167	Sodium Ion Binding Pocket Mutations and Adenosine A_{2A}Receptor Function. Molecular Pharmacology, 2015, 87, 305-313.	1.0	79
168	A Single-Domain Llama Antibody Potently Inhibits the Enzymatic Activity of Botulinum Neurotoxin by Binding to the Non-Catalytic Î±-Exosite Binding Region. Journal of Molecular Biology, 2010, 397, 1106-1118.	2.0	78
169	Structure-Based Ligand Discovery Targeting Orthosteric and Allosteric Pockets of Dopamine Receptors. Molecular Pharmacology, 2013, 84, 794-807.	1.0	78
170	Crystal structure of the Frizzled 4 receptor in a ligand-free state. Nature, 2018, 560, 666-670.	13.7	77
171	Crystal Structure and DNA Binding of the Homeodomain of the Stem Cell Transcription Factor Nanog. Journal of Molecular Biology, 2008, 376, 758-770.	2.0	76
172	Nuclear Magnetic Resonance Structure of the N-Terminal Domain of Nonstructural Protein 3 from the Severe Acute Respiratory Syndrome Coronavirus. Journal of Virology, 2007, 81, 12049-12060.	1.5	75
173	A Comparative Analysis of the Immunological Evolution of Antibody 28B4. Biochemistry, 2001, 40, 10764-10773.	1.2	73
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